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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jongsma, Maarten Anthonie
Strukelj, Borut
Lenarcic, Brigita
Gruden, Kristina
Turk, Vito
Bosch, Hendrik J.
Stiekema, Willem Johannes
- (ii) TITLE OF INVENTION: A Method for Plant Protection Against Insects
or Nematodes
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DLO-Center for Plant Breeding and
Reproduction Research
 - (B) STREET: Droevendaalsesteeg 1
 - (C) CITY: Wageningen
 - (D) STATE: N/A
 - (E) COUNTRY: The Netherlands
 - (F) ZIP (POSTAL CODE): 6708 PB
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 Floppy disk, 1.44 MB
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/445,480
 - (B) FILING DATE: July 7, 2000
 - (C) CLASSIFICATION: C12N15/82
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/NL98/00352
 - (B) FILING DATE: June 18, 1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: McCLURE, DANIEL R.
 - (B) REGISTRATION NUMBER: 38,962
 - (C) REFERENCE/DOCKET NUMBER: 250308-1020
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: +31 317 477001
 - (B) TELEFAX: +31 317 418094

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinia equina*

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 99..695

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..695

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 3..98

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..2

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 696..888

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Gruden, Kristina
Strukelj, Borut
Popovic, Tatjana
Lenarcic, Brigita
Bevec, Tadeja
Brzin, Joze
Kregar, Igor
Herzog-Velikonja, Jana
Stiekema, Willem J
Bosch, Dirk
- (B) TITLE: The Cysteine Protease Activity of Colorado
Potato Beetle (*Leptinotarsa decemlineata*) Guts,
Which is Insensitive to Potato Protease
Inhibitors, is Inhibited by Thyroglobulin Type-1
Domain Inhibitors
- (C) JOURNAL: Insect Biochem. Mol. Biol
- (D) VOLUME: 28
- (F) PAGES: 549-560
- (G) DATE: 1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CT ATG GCT CTT AGC CAA AAC CAA GCC AAG TTT TCC AAA GGA TTC GTC	47
Met Ala Leu Ser Gln Asn Gln Ala Lys Phe Ser Lys Gly Phe Val	
-32 -30 -25 -20	
GTG ATG ATT TGG GTA CTA TTC ATT GCT TGT GCT ATA ACT TCA ACT GAA	95
Val Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Glu	
-15 -10 -5	
GCT AGT CTA ACC AAA TGC CAA CAG CTC CAG GCC TCG GCT AAC AGT GGT	143
Ala Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly	
1 5 10 15	
CTG ATA GGT ACT TAT GTA CCA CAA TGC AAA GAA ACG GGA GAG TTC GAA	191
Leu Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu	
20 25 30	
GAA AAA CAA TGC TGG GGA TCG ACT GGT TAC TGT TGG TGT GTG GAT GAA	239
Glu Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val Asp Glu	
35 40 45	
GAT GGA AAA GAG ATT CTA GGA ACC AAG ATC CGT GGA TCT CCG GAT TGC	287
Asp Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys	
50 55 60	
AGC CGC AGA AAA GCC GCG TTA ACA CTT TGC CAG ATG ATG CAA GCC ATC	335
Ser Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile	
65 70 75	
ATT GTT AAT GTC CCT GGT TGG TGT GGC CCT CCA TCG TGT AAA GCT GAC	383
Ile Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp	
80 85 90 95	
GGC AGT TTT GAC GAG GTT CAG TGC TGC GCA AGT AAT GGA GAA TGC TAC	431
Gly Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr	
100 105 110	
TGT GTG GAT AAG AAA GGA AAA GAA CTT GAA GGC ACA AGA CAA CAG GGA	479
Cys Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly	
115 120 125	
AGG CCA ACC TGC GAA AGA CAC CTA AGC GAA TGC GAG GAA GCT CGA ATC	527
Arg Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Glu Ala Arg Ile	
130 135 140	
AAG GCG CAT TCA AAC AGT CTT CGT GTT GAG ATG TTC GTG CCA GAG TGT	575
Lys Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys	
145 150 155	
TTA GAA GAT GGA TCA TAT AAC CCA GTA CAG TGC TGG CCT AGC ACA GGA	623
Leu Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly	
160 165 170 175	
TAC TGT TGG TGC GTC GAT GAA GGA GGG GTA AAG GTA CCA GGT TCC GAT	671
Tyr Cys Trp Cys Val Asp Glu Gly Gly Val Lys Val Pro Gly Ser Asp	

180	185	190	
GTC AGA TTT AAA CGC CCC ACA TGC TAAGAAAAAC ACAGTGAACA AAGTGGCTAG			725
Val Arg Phe Lys Arg Pro Thr Cys			
195			
TTTCCAGATC GAAAATAACT ACAAAGGATT AATAAAATGT TAAAATAATT TCTCAATTTCG			785
GCTGTGATAT ATTTTTTCCA AGATAATTTA ATCTGCATGT AGTTAACAGA AAACAATCTC			845
AACTAGAAAT AAAGACTACG GTAATAATGA CAAAAA AAA			888

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Leu	Ser	Gln	Asn	Gln	Ala	Lys	Phe	Ser	Lys	Gly	Phe	Val	Val	
-32		-30					-25					-20				
Met	Ile	Trp	Val	Leu	Phe	Ile	Ala	Cys	Ala	Ile	Thr	Ser	Thr	Glu	Ala	
-15						-10					-5					
Ser	Leu	Thr	Lys	Cys	Gln	Gln	Leu	Gln	Ala	Ser	Ala	Asn	Ser	Gly	Leu	
1				5					10					15		
Ile	Gly	Thr	Tyr	Val	Pro	Gln	Cys	Lys	Glu	Thr	Gly	Glu	Phe	Glu	Glu	
			20					25					30			
Lys	Gln	Cys	Trp	Gly	Ser	Thr	Gly	Tyr	Cys	Trp	Cys	Val	Asp	Glu	Asp	
		35					40					45				
Gly	Lys	Glu	Ile	Leu	Gly	Thr	Lys	Ile	Arg	Gly	Ser	Pro	Asp	Cys	Ser	
50						55					60					
Arg	Arg	Lys	Ala	Ala	Leu	Thr	Leu	Cys	Gln	Met	Met	Gln	Ala	Ile	Ile	
65					70					75					80	
Val	Asn	Val	Pro	Gly	Trp	Cys	Gly	Pro	Pro	Ser	Cys	Lys	Ala	Asp	Gly	
				85				90						95		
Ser	Phe	Asp	Glu	Val	Gln	Cys	Cys	Ala	Ser	Asn	Gly	Glu	Cys	Tyr	Cys	
		100						105					110			
Val	Asp	Lys	Lys	Gly	Lys	Glu	Leu	Glu	Gly	Thr	Arg	Gln	Gln	Gly	Arg	
		115					120					125				
Pro	Thr	Cys	Glu	Arg	His	Leu	Ser	Glu	Cys	Glu	Glu	Ala	Arg	Ile	Lys	
130						135					140					
Ala	His	Ser	Asn	Ser	Leu	Arg	Val	Glu	Met	Phe	Val	Pro	Glu	Cys	Leu	

[illegible]

ATA GGT ACT TAT GTA CCA CAA TGC AAA GAA ACT GGA GAG TTT GAA GAA Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu Glu 20 25 30	192
AAG CAA TGC TGG GGA TCG ACT GGT TAC TGT TGG TGT GTG GAT GAA GAT Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val Asp Glu Asp 35 40 45	240
GGA AAA GAG ATT CTA GGT ACA AAG ATC CGT GGA TCT CCA GAC TGC AGT Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys Ser 50 55 60	288
CGC AGA AAA GCT GCC TTA ACA CTT TGC CAG ATG ATG CAA GCC ATC ATT Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile Ile 65 70 75 80	336
GTG AAT GTC CCT GGT TGG TGT GGA CCT CCA TCA TGT AAA GCT GAC GGC Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp Gly 85 90 95	384
AGT TTT GAC GAG GTT CAG TGC TGC GCA AGT AAT GGA GAA TGC TAC TGT Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr Cys 100 105 110	432
GTG GAT AAG AAA GGA AAA GAA CTT GAA GGC ACA AGA CAA CAG GGA AGG Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly Arg 115 120 125	480
CCA ACC TGC GAA AGA CAC CTA AGC GAA TGC GAG GAG GCT CGT ATC AAG Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Glu Ala Arg Ile Lys 130 135 140	528
GCA CAT TCA AAC AGT CTT CGT GTT GAG ATG TTC GTG CCA GAG TGT TTA Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys Leu 145 150 155 160	576
GAA GAT GGA TCT TAC AAC CCT GTA CAG TGC TGG CCT AGC ACA GGA TAC Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly Tyr 165 170 175	624
TGT TGG TGC GTC GAT GAA GGA GGG GTA AAG GTT CCA GGT TCC GAC GTC Cys Trp Cys Val Asp Glu Gly Gly Val Lys Val Pro Gly Ser Asp Val 180 185 190	672
AGA TTC AAA CGT CCC ACA TGC TAA Arg Phe Lys Arg Pro Thr Cys 195	696

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Leu Ser Gln Asn Gln Ala Lys Phe Ser Lys Gly Phe Val Val
-32 -30 -25 -20
Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Glu Ala
-15 -10 -5
Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly Leu
1 5 10 15
Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu Glu
20 25 30
Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val Asp Glu Asp
35 40 45
Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys Ser
50 55 60
Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile Ile
65 70 75 80
Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp Gly
85 90 95
Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr Cys
100 105 110
Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly Arg
115 120 125
Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Glu Ala Arg Ile Lys
130 135 140
Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys Leu
145 150 155 160
Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly Tyr
165 170 175
Cys Trp Cys Val Asp Glu Gly Gly Val Lys Val Pro Gly Ser Asp Val
180 185 190
Arg Phe Lys Arg Pro Thr Cys
195